

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1 - 5. (Canceled)

6. (Currently amended) The method of claim 8, wherein the DNA methylation pattern for the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus and the differentiation state-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

7. (Canceled)

8. (Currently amended) A method of identifying the differentiation state of a test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus, wherein the test cell, test tissue, or test nucleus is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a stem cell tissue, and a nucleus differentiated from a stem cell nucleus comprising:

obtaining a DNA methylation pattern for the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus, wherein the DNA methylation pattern for the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a differentiation state-specific DNA methylation pattern for one or more ~~stem~~-cell, ~~stem~~-cell-tissue, or ~~stem~~-cell-nucleus of known differentiation state, wherein the one or more cell, tissue, or nucleus of known differentiation state is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a stem cell tissue, and a nucleus differentiated from a stem cell nucleus; and,

comparing the DNA methylation pattern for the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus with the differentiation state-specific DNA methylation pattern,

wherein the differentiation state of the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus is identified if the DNA methylation pattern of the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus matches the differentiation state-specific DNA methylation pattern.

9. (Previously presented) The method of claim 8, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

10 - 18. (Canceled)

19. (Currently amended) The method of claim 8, wherein the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus is an embryonic stem cell, embryonic stem cell tissue, or embryonic stem cell nucleus, differentiating embryonic stem cell, differentiating embryonic stem cell tissue, differentiating embryonic stem cell nucleus, a cell differentiated from an embryonic stem cell, a tissue differentiated from an embryonic stem cell tissue, or a nucleus differentiated from an embryonic stem cell nucleus.

20. (Currently amended) The method of claim 8, wherein the differentiation state of the one or more ~~stem~~-cell, ~~stem~~-cell-tissue, or ~~stem~~-cell-nucleus of known differentiation state is differentiated.

21. (Currently amended) The method of claim 8, wherein the differentiation state of the one or more ~~stem~~-cell, ~~stem~~-cell-tissue, or ~~stem~~-cell-nucleus of known differentiation state is undifferentiated.

22. (Currently amended) A method of identifying a test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus, wherein the test cell, test tissue, or test nucleus is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem

cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a stem cell tissue, and a nucleus differentiated from a stem cell nucleus, comprising:

obtaining a DNA methylation pattern for the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus, wherein the DNA methylation pattern for the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a cell-, tissue-, or nucleus-specific DNA methylation pattern for one or more known types of ~~stem~~-cell, ~~stem~~-cell-tissue, or ~~stem~~-cell-nucleus; wherein the one or more known types of ~~stem~~-cell, ~~stem~~-cell-tissue, or ~~stem~~-cell-nucleus is selected from undifferentiated embryonic stem cell, differentiated-differentiating embryonic stem cell, cell differentiated from embryonic stem cell, undifferentiated trophoblast stem cell, and differentiated-differentiating trophoblast stem cell, and cell differentiated from trophoblast stem cell; and,

comparing the DNA methylation pattern for the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus with the cell-, tissue-, or nucleus-specific DNA methylation pattern of the known ~~stem~~-cell, ~~stem~~-cell-tissue, or ~~stem~~-cell nucleus to permit identification of the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus as one of the known types of ~~stem~~-cell, ~~stem~~-cell-tissue, or ~~stem~~-cell nucleus;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated embryonic stem cell identifies the

test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus as undifferentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiateddifferentiating embryonic stem cell identifies the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus as differentiateddifferentiating embryonic stem cell;

wherein a match to the cell-, tissue-, or
nucleus-specific DNA methylation pattern of the
cell differentiated from embryonic stem cell
identifies the test cell, test tissue, or test nucleus as
differentiated from embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated trophoblast stem cell identifies the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus as undifferentiated trophoblast stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiateddifferentiating trophoblast stem cell identifies the test ~~stem~~-cell, test ~~stem~~-cell-tissue, or test ~~stem~~-cell-nucleus as differentiateddifferentiating trophoblast stem cell;

wherein a match to the cell-, tissue-, or
nucleus-specific DNA methylation pattern of the
cell differentiated from trophoblast stem cell
identifies the test cell, test tissue, or test nucleus as
differentiated from trophoblast stem cell.

23. (Previously presented) The method of claim 22, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

24. (New) The method of claim 8, wherein the differentiation state of the one or more cell, tissue, or nucleus of known differentiation state is differentiating.